1/19



SEQUENCE LISTING

<110> HOOD, John ELICEIRI, Brian CHERESH, David <120> Methods and Compositions Useful for Modulation of Angiogenesis Using Tyrosine Kinase Raf and Ras <130> TSRI 710.2 <140> 09/637,302 <141> 2000-08-11 <150> US 60/148,924 <151> 1999-08-13 <150> US 60/215,951 <151> 2000-07-05 <160> 7 <170> PatentIn Ver. 2.0 <210> 1 <211> 2977 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (130)..(2073) <400> 1 ccgaatgtga ccgcctcccg ctccctcacc cgccgcgggg aggaggagcg ggcgagaagc 60 tgccgccgaa cgacaggacg ttggggcggc ctggctccct caggtttaag aattgtttaa 120 gctgcatca atg gag cac ata cag gga gct tgg aag acg atc agc aat ggt 171 Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly 1 10 ttt gga ttc aaa gat gcc gtg ttt gat ggc tcc agc tgc atc tct cct Phe Gly Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro 15 20 aca ata gtt cag cag ttt ggc tat cag cgc cgg gca tca gat gat ggc 267 Thr Ile Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly 35 aaa ctc aca gat cct tct aag aca agc aac act atc cgt gtt ttc ttg 315 Lys Leu Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu 50 60

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Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys 85 90 95

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- Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly 290 295 300
- Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro 305 310 315 320
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<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Artificial Sequence

<sup>&</sup>lt;220>

<sup>&</sup>lt;223> Description of Artificial Sequence: fusion protein

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

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aca Thr	gat Asp 50	cct Pro	tct Ser	aag Lys	aca Thr	agc Ser 55	aac Asn	act Thr	atc Ile	cgt Arg	gtt Val 60	ttc Phe	ttg Leu	ccg Pro	aac Asn	192
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1296

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- Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val 260 265 270
- Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala 275 280 285
- Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly 290 295 300
- Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro 305 310 315 320
- Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg 325 330 335
- Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser 340 350
- Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp 355 360 365
- His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro 370 375 380
- Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr 385 390 395 400
- Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn 405 410 415
- Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His 420 425 430
- Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile 435 440 445
- Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile 450 455 460
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500 505 510

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